



PATENT

Our Docket: P-IX 4143

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

Lockridge and Watkins

Serial No.: 09/748,739

Filed: December 26, 2000

For: BUTYRYLCHOLINESTERASE
VARIANTS AND METHODS
OF USE

Group Art Unit: 1623

Examiner: Not yet Assigned

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Box Missing Parts, Commissioner for Patents, Washington, D.C. 20231, on May 30, 2001.

Bv

Astrid R. Spain, Reg. No. 47,956

May 30, 2001

Date of Signature

Box Missing Parts
Commissioner for Patents
Washington, D.C. 20231

Sir:

STATEMENT UNDER 37 C.F.R. § 1.821(f) and (g)

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 CFR § 1.821(c) and (e), respectively, are the same.

I hereby state that the submission, filed in accordance with 37 C.F.R. § 1.821(g) herein does not include new matter.

Respectfully submitted,

May 30, 2001

Date

Kind R. 800m

Astrid R. Spain

Registration No. 47,956

Telephone: (858) 535-9001

Facsimile: (858) 535-8949

CAMPBELL & FLORES LLP
4370 La Jolla Village Drive
7th Floor
San Diego, California 92122
USPTO CUSTOMER NO. 23601



SEQUENCE LISTING

<110> Lockridge, Oksana
Watkins, Jeffry D.

<120> Butyrylcholinesterase Variants and Methods of Use

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65 70 75 80
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn
85 90 95
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Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
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Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
				260					265					270	
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Gly	Val
				275				280					285		
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
				290			295				300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310					315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly
				325					330					335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
				340					345					350	
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser
				355				360					365		
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn
				370			375				380				
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys
385					390					395					400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala
				405					410					415	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu
				420					425					430	
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu
				435				440					445		
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser
				450			455				460				
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro
465					470					475					480
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr
				485					490					495	
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr
				500				505					510		
Lys	Leu	Arg													

<213> Artificial Sequence

<223> Human Butyrylcholinesterase variant

<222> (214) ... (1935)

tactgaatgt	cagtcgagtc	caatttacag	gctggagcag	cagctgcac	ctgcatttcc	60
ccgaagtatt	acatgatttt	cactccttgc	aaactttacc	atctttgttg	cagagaatcg	120
gaaatcaata	tgcatagcaa	agtcacaatc	atatgcatca	gattttctctt	ttggtttctt	180
ttgctctgca	tgcttattgg	gaagtcacat	act gaa gat	gac atc ata	att gca	234
			Glu Asp Asp	Ile Ile Ile	Ala	
			1	5		

acg gta aca gcc ttt ctt gga att ccc tat gca cag cca cct ctt ggt 330
Thr Val Thr Ala Phe Leu Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly
25 30 35

aga ctt cga ttc aaa aag cca cag tct ctg acc aag tgg tct gat att 378
Arg Leu Arg Phe Lys Lys Pro Gln Ser Leu Thr Lys Trp Ser Asp Ile
40 45 50 55

tgg aat gcc aca aaa tat gca aat tct tgc tgt cag aac ata gat caa 426
 Trp Asn Ala Thr Lys Tyr Ala Asn Ser Cys Cys Gln Asn Ile Asp Gln
 60 65 70

[illegible]

ctc agt gaa gac tgt tta tat cta aat gta tgg att cca gca cct aaa 522
Leu Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ile Pro Ala Pro Lys
90 95 100

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cca aaa aat gcc act gta ttg ata tgg att tat ggt ggt ggt ttt caa    570
Pro Lys Asn Ala Thr Val Leu Ile Trp Ile Tyr Gly Gly Gly Phe Gln
      105                110                115
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act gga aca tca tct tta cat gtt tat gat ggc aag ttt ctg gct cgg 618
Thr Gly Thr Ser Ser Leu His Val Tyr Asp Gly Lys Phe Leu Ala Arg
120 125 130 135

gtt gaa aqa gtt att qta qtq tca atq aac tat aqq qtq qgt qcc cta 666

Val Glu Arg Val Ile Val Val Ser Met Asn Tyr Arg Val Gly Ala Leu	
140 145 150	
gga ttc tta gct ttg cca gga aat cct gag gct cca ggg aac atg ggt	714
Gly Phe Leu Ala Leu Pro Gly Asn Pro Glu Ala Pro Gly Asn Met Gly	
155 160 165	
tta ttt gat caa cag ttg gct ctt cag tgg gtt caa aaa aat ata gca	762
Leu Phe Asp Gln Gln Leu Ala Leu Gln Trp Val Gln Lys Asn Ile Ala	
170 175 180	
gcc ttt ggt gga aat cct aaa agt gta act ctc ttt gga gaa agt gca	810
Ala Phe Gly Gly Asn Pro Lys Ser Val Thr Leu Phe Gly Glu Ser Ala	
185 190 195	
gga gca gct tca gtt agc ctg cat ttg ctt tct cct gga agc cat tca	858
Gly Ala Ala Ser Val Ser Leu His Leu Leu Ser Pro Gly Ser His Ser	
200 205 210 215	
ttg ttc acc aga gcc att ctg caa agt gga tcc ttt aat gct cct tgg	906
Leu Phe Thr Arg Ala Ile Leu Gln Ser Gly Ser Phe Asn Ala Pro Trp	
220 225 230	
gcg gta aca tct ctt tat gaa gct agg aac aga acg ttg aac tta gct	954
Ala Val Thr Ser Leu Tyr Glu Ala Arg Asn Arg Thr Leu Asn Leu Ala	
235 240 245	
aaa ttg act ggt tgc tct aga gag aat gag act gaa ata atc aag tgt	1002
Lys Leu Thr Gly Cys Ser Arg Glu Asn Glu Thr Glu Ile Ile Lys Cys	
250 255 260	
ctt aga aat aaa gat ccc caa gaa att ctt ctg aat gaa gca ttt gtt	1050
Leu Arg Asn Lys Asp Pro Gln Glu Ile Leu Leu Asn Glu Ala Phe Val	
265 270 275	
gtc ccc tat ggg act cag ttg tca gta aac ttt ggt ccg acc gtg gat	1098
Val Pro Tyr Gly Thr Gln Leu Ser Val Asn Phe Gly Pro Thr Val Asp	
280 285 290 295	
ggt gat ttt ctc act gac atg cca gac ata tta ctt gaa ctt gga caa	1146
Gly Asp Phe Leu Thr Asp Met Pro Asp Ile Leu Leu Glu Leu Gly Gln	
300 305 310	
ttt aaa aaa acc cag att ttg gtg ggt gtt aat aaa gat gaa ggg aca	1194
Phe Lys Lys Thr Gln Ile Leu Val Gly Val Asn Lys Asp Glu Gly Thr	
315 320 325	
gct ttt tta gtc tat ggt gct cct ggc ttc agc aaa gat aac aat agt	1242
Ala Phe Leu Val Tyr Gly Ala Pro Gly Phe Ser Lys Asp Asn Asn Ser	
330 335 340	
atc ata act aga aaa gaa ttt cag gaa ggt tta aaa ata ttt ttt cca	1290
Ile Ile Thr Arg Lys Glu Phe Gln Glu Gly Leu Lys Ile Phe Phe Pro	

345	350	355	
gga gtg agt gag ttt gga aag gaa tcc atc ctt ttt cat tac aca gac			1338
Gly Val Ser Glu Phe Gly Lys Glu Ser Ile Leu Phe His Tyr Thr Asp			
360	365	370	375
tggtta gat gat cag aga cct gaa aac tac cgt gag gcc ttg ggt gat			1386
Trp Val Asp Asp Gln Arg Pro Glu Asn Tyr Arg Glu Ala Leu Gly Asp			
380	385		390
gtt gtt ggg gat tat aat ttc ata tgc cct gcc ttg gag ttc acc aag			1434
Val Val Gly Asp Tyr Asn Phe Ile Cys Pro Ala Leu Glu Phe Thr Lys			
395	400		405
aag ttc tca gaa tgg gga aat aat gcc ttt ttc tac tat ttt gaa cac			1482
Lys Phe Ser Glu Trp Gly Asn Asn Ala Phe Phe Tyr Tyr Phe Glu His			
410	415		420
cga tcc tcc aaa ctt ccg tgg cca gaa tgg atg gga gtg atg cat ggc			1530
Arg Ser Ser Lys Leu Pro Trp Pro Glu Trp Met Gly Val Met His Gly			
425	430		435
tat gaa att gaa ttt gtc ttt ggt tta cct ctg gaa aga aga gat aat			1578
Tyr Glu Ile Glu Phe Val Phe Gly Leu Pro Leu Glu Arg Arg Asp Asn			
440	445		450
tac aca aaa gcc gag gaa att ttg agt aga tcc ata gtg aaa cgg tgg			1626
Tyr Thr Lys Ala Glu Glu Ile Leu Ser Arg Ser Ile Val Lys Arg Trp			
460	465		470
gca aat ttt gca aaa tat ggg aat cca aat gag act cag aac aat agc			1674
Ala Asn Phe Ala Lys Tyr Gly Asn Pro Asn Glu Thr Gln Asn Asn Ser			
475	480		485
aca agc tgg cct gtc ttc aaa agc act gaa caa aaa tat cta acc ttg			1722
Thr Ser Trp Pro Val Phe Lys Ser Thr Glu Gln Lys Tyr Leu Thr Leu			
490	495		500
aat aca gag tca aca aga ata atg acg aaa cta cgt gct caa caa tgt			1770
Asn Thr Glu Ser Thr Arg Ile Met Thr Lys Leu Arg Ala Gln Gln Cys			
505	510		515
cga ttc tgg aca tca ttt ttt cca aaa gtc ttg gaa atg aca gga aat			1818
Arg Phe Trp Thr Ser Phe Phe Pro Lys Val Leu Glu Met Thr Gly Asn			
520	525		530
att gat gaa gca gaa tgg gag tgg aaa gca gga ttc cat cgc tgg aac			1866
Ile Asp Glu Ala Glu Trp Glu Trp Lys Ala Gly Phe His Arg Trp Asn			
540	545		550
aat tac atg atg gac tgg aaa aat caa ttt aac gat tac act agc aag			1914
Asn Tyr Met Met Asp Trp Lys Asn Gln Phe Asn Asp Tyr Thr Ser Lys			
555	560		565

TOP SECRET - CONFIDENTIAL

attttccttt	agatcaaggc	aaaaatatca	ggagcttttt	tacacaccta	ctaaaaaagt	2025
tattatgtag	ctgaaacaaa	aatgccagaa	ggataatatt	gattcctcac	atctttaact	2085
tagtatttta	cctagcattt	caaaacccaa	atggctagaa	catgtttaat	taaatttcac	2145
aatataaagt	tctacagtta	attatgtgca	tattaaaaca	atggcctggg	tcaatttctt	2205
tctttcctta	ataaatttaa	gttttttccc	cccaaaatta	tcagtgtctt	gcttttagtc	2265
acgtgtattt	tcattaccac	tcgtaaaaag	gtatcttttt	taaatagaatt	aaatattgaa	2325
acactgtaca	ccatagttta	caatattatg	tttcctaatt	aaaataagaa	ttgaatgtca	2385
atatgagata	ttaaaataag	cacagaaaaat	c			2416

<213> Artificial Sequence

<223> Human Butyrylcholinesterase variant

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met
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Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro
			20					25					30		
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser
		35					40					45			
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
	50					55					60				
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
65				70						75					80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
			85						90					95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100					105					110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
		115					120					125			
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
	130					135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145				150						155					160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
			165						170					175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
		195					200					205			
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210					215					220				
Gly	Ser	Phe	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225				230						235					240

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Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn
      245                      250                      255
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile
      260                      265                      270
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Gln Leu Ser Val
      275                      280                      285
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp
      290                      295                      300
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly
305                      310                      315                      320
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly
      325                      330                      335
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu
      340                      345                      350
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser
      355                      360                      365
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn
      370                      375                      380
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys
385                      390                      395                      400
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala
      405                      410                      415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
      420                      425                      430
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu
      435                      440                      445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
      450                      455                      460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
465                      470                      475                      480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
      485                      490                      495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
      500                      505                      510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
      515                      520                      525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
      530                      535                      540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
545                      550                      555                      560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
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<210> 7

<211> 2416

<212> DNA

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<221> CDS

<400> 7

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Thr Lys Asn Gly Lys Val Arg Gly Met Asn Leu Thr Val Phe Gly Gly
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acg gta aca gcc ttt ctt gga att ccc tat gca cag cca cct ctt ggt 330
Thr Val Thr Ala Phe Leu Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly
25 30 35

aga ctt cga ttc aaa aag cca cag tct ctg acc aag tgg tct gat att 378
Arg Leu Arg Phe Lys Lys Pro Gln Ser Leu Thr Lys Trp Ser Asp Ile
40 45 50 55

tgg aat gcc aca aaa tat gca aat tct tgc tgt cag aac ata gat caa 426
 Trp Asn Ala Thr Lys Tyr Ala Asn Ser Cys Cys Gln Asn Ile Asp Gln
 60 65 70

agt ttt cca ggc ttc cat gga tca gag atg tgg aac cca aac act gac 474
 Ser Phe Pro Gly Phe His Gly Ser Glu Met Trp Asn Pro Asn Thr Asp
 75 80 85

ctc agt gaa gac tgt tta tat cta aat gta tgg att cca gca cct aaa 522
Leu Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ile Pro Ala Pro Lys
90 95 100

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cca aaa aat gcc act gta ttg ata tgg att tat ggt ggt ggt ttt caa    570
Pro Lys Asn Ala Thr Val Leu Ile Trp Ile Tyr Gly Gly Gly Phe Gln
      105                110                115
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act gga aca tca tct tta cat gtt tat gat ggc aag ttt ctg gct cgg 618
Thr Gly Thr Ser Ser Leu His Val Tyr Asp Gly Lys Phe Leu Ala Arg
120 125 130 135

gtt gaa aga gtt att gta gtg tca atg aac tat agg gtg ggt gcc cta 666
Val Glu Arg Val Ile Val Val Ser Met Asn Tyr Arg Val Gly Ala Leu
140 145 150

gga ttc tta gct ttg cca gga aat cct gag gct cca ggg aac atg ggt 714
Gly Phe Leu Ala Leu Pro Gly Asn Pro Glu Ala Pro Gly Asn Met Gly
155 160 165

tta ttt gat caa cag ttg gct ctt cag tgg gtt caa aaa aat ata gca 762
Leu Phe Asp Gln Gln Leu Ala Leu Gln Trp Val Gln Lys Asn Ile Ala
170 175 180

gcc ttt ggt gga aat cct aaa agt gta act ctc ttt gga gaa agt gca	810
Ala Phe Gly Gly Asn Pro Lys Ser Val Thr Leu Phe Gly Glu Ser Ala	
185 190 195	
gga gca gct tca gtt agc ctg cat ttg ctt tct cct gga agc cat tca	858
Gly Ala Ala Ser Val Ser Leu His Leu Leu Ser Pro Gly Ser His Ser	
200 205 210 215	
ttg ttc acc aga gcc att ctg caa agt gga tcc ttt aat gct cct tgg	906
Leu Phe Thr Arg Ala Ile Leu Gln Ser Gly Ser Phe Asn Ala Pro Trp	
220 225 230	
gcg gta aca tct ctt tat gaa gct agg aac aga acg ttg aac tta gct	954
Ala Val Thr Ser Leu Tyr Glu Ala Arg Asn Arg Thr Leu Asn Leu Ala	
235 240 245	
aaa ttg act ggt tgc tct aga gag aat gag act gaa ata atc aag tgt	1002
Lys Leu Thr Gly Cys Ser Arg Glu Asn Glu Thr Glu Ile Ile Lys Cys	
250 255 260	
ctt aga aat aaa gat ccc caa gaa att ctt ctg aat gaa gca ttt gtt	1050
Leu Arg Asn Lys Asp Pro Gln Glu Ile Leu Leu Asn Glu Ala Phe Val	
265 270 275	
gtc ccc tat ggg act tcg ttg tca gta aac ttt ggt ccg acc gtg gat	1098
Val Pro Tyr Gly Thr Ser Leu Ser Val Asn Phe Gly Pro Thr Val Asp	
280 285 290 295	
ggt gat ttt ctc act gac atg cca gac ata tta ctt gaa ctt gga caa	1146
Gly Asp Phe Leu Thr Asp Met Pro Asp Ile Leu Leu Glu Leu Gly Gln	
300 305 310	
ttt aaa aaa acc cag att ttg gtg ggt gtt aat aaa gat gaa ggg aca	1194
Phe Lys Lys Thr Gln Ile Leu Val Gly Val Asn Lys Asp Glu Gly Thr	
315 320 325	
gct ttt tta gtc tat ggt gct cct ggc ttc agc aaa gat aac aat agt	1242
Ala Phe Leu Val Tyr Gly Ala Pro Gly Phe Ser Lys Asp Asn Asn Ser	
330 335 340	
atc ata act aga aaa gaa ttt cag gaa ggt tta aaa ata ttt ttt cca	1290
Ile Ile Thr Arg Lys Glu Phe Gln Glu Gly Leu Lys Ile Phe Phe Pro	
345 350 355	
gga gtg agt gag ttt gga aag gaa tcc atc ctt ttt cat tac aca gac	1338
Gly Val Ser Glu Phe Gly Lys Glu Ser Ile Leu Phe His Tyr Thr Asp	
360 365 370 375	
tgg gta gat gat cag aga cct gaa aac tac cgt gag gcc ttg ggt gat	1386
Trp Val Asp Asp Gln Arg Pro Glu Asn Tyr Arg Glu Ala Leu Gly Asp	
380 385 390	

gtt gtt ggg gat tat aat ttc ata tgc cct gcc ttg gag ttc acc aag 1434
Val Val Gly Asp Tyr Asn Phe Ile Cys Pro Ala Leu Glu Phe Thr Lys
395 400 405

aag ttc tca gaa tgg gga aat aat gcc ttt ttc tac tat ttt gaa cac 1482
Lys Phe Ser Glu Trp Gly Asn Asn Ala Phe Phe Tyr Tyr Phe Glu His
410 415 420

cga tcc tcc aaa ctt ccg tgg cca gaa tgg atg gga gtg atg cat ggc 1530
Arg Ser Ser Lys Leu Pro Trp Pro Glu Trp Met Gly Val Met His Gly
425 430 435

tat gaa att gaa ttt gtc ttt ggt tta cct ctg gaa aga aga gat aat 1578
Tyr Glu Ile Glu Phe Val Phe Gly Leu Pro Leu Glu Arg Arg Asp Asn
440 445 450 455

tac aca aaa gcc gag gaa att ttg agt aga tcc ata gtg aaa cgg tgg 1626
Tyr Thr Lys Ala Glu Glu Ile Leu Ser Arg Ser Ile Val Lys Arg Trp
460 465 470

gca aat ttt gca aaa tat ggg aat cca aat gag act cag aac aat agc 1674
Ala Asn Phe Ala Lys Tyr Gly Asn Pro Asn Glu Thr Gln Asn Asn Ser
475 480 485

aca agc tgg cct gtc ttc aaa agc act gaa caa aaa tat cta acc ttg 1722
Thr Ser Trp Pro Val Phe Lys Ser Thr Glu Gln Lys Tyr Leu Thr Leu
490 495 500

aat aca gag tca aca aga ata atg acg aaa cta cgt gct caa caa tgt 1770
Asn Thr Glu Ser Thr Arg Ile Met Thr Lys Leu Arg Ala Gln Gln Cys
505 510 515

cga ttc tgg aca tca ttt ttt cca aaa gtc ttg gaa atg aca gga aat 1818
Arg Phe Trp Thr Ser Phe Phe Pro Lys Val Leu Glu Met Thr Gly Asn
520 525 530 535

att gat gaa gca gaa tgg gag tgg aaa gca gga ttc cat cgc tgg aac 1866
Ile Asp Glu Ala Glu Trp Glu Trp Lys Ala Gly Phe His Arg Trp Asn
540 545 550

aat tac atg atg gac tgg aaa aat caa ttt aac gat tac act agc aag 1914
Asn Tyr Met Met Asp Trp Lys Asn Gln Phe Asn Asp Tyr Thr Ser Lys
555 560 565

aaa gaa agt tgt gtg ggt ctc taattaatag atttaccctt tatagaacat 1965
Lys Glu Ser Cys Val Gly Leu
570

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tattatgtag ctgaaacaaa aatgccagaa ggataatatt gattcctcac atctttaact 2085
tagtatttta cctagcattt caaaacccaa atggctagaa catgtttaat taaatttcac 2145
aatataaagt tctacagtta attatgtgca tattaaaaca atggcctggg tcaatttcctt 2205
tctttcctta ataaatttaa gttttttccc cccaaaatta tcagtgtctt gcttttagtc 2265

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<210> 8
<211> 574
<212> PRT
<213> Artificial Sequence
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			20					25					30			
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	
		35					40					45				
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	
	50					55					60					
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	
65				70						75				80		
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	
				85					90					95		
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	
			100					105					110			
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	
		115					120					125				
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	
	130					135					140					
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	
145				150						155				160		
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	
				165					170					175		
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	
			180					185					190			
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	
		195					200					205				
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	
	210					215					220					
Gly	Ser	Phe	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	
225				230						235				240		
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
				245					250					255		
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Ser	Leu	Ser	Val	
		275					280					285				
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
		290				295						300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310						315				320	

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Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly
      325                      330                      335
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu
      340                      345                      350
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser
      355                      360                      365
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn
      370                      375                      380
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys
      385                      390                      395                      400
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala
      405                      410                      415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
      420                      425                      430
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu
      435                      440                      445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
      450                      455                      460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
      465                      470                      475                      480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
      485                      490                      495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
      500                      505                      510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
      515                      520                      525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
      530                      535                      540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
      545                      550                      555                      560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
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<210> 9

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<400> 9

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Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu Met Trp
  1                      5                      10                      15

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<210> 10

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<400> 10

Leu Ile Trp Ile Tyr Gly Gly Gly Phe Gln Thr Gly
1 5 10

<210> 11

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<400> 11

Leu Phe Gly Glu Ser Ala Gly Ala
1 5

<210> 12

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<400> 12

Ser Gly Ser Phe Asn Ala Pro Trp Ala Val Thr
1 5 10

<210> 13

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<400> 13

Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val Asn
1 5 10

<210> 14

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

TEBEBE"BEED

<400> 14

Thr Ala Phe Leu Val Tyr

1 5

<210> 15

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<400> 15

Pro Trp Pro Glu Trp Met Gly Val Met His Gly Tyr Glu Ile

1 5 10

<210> 16

<211> 2416

<212> DNA

<213> Homo sapiens

<400> 16

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gaaatcaata tgcatagcaa agtcacaatc atatgcatca gatttctctt ttggtttctt 180
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tcagaatggg gaaataatgc cttttttctac tattttgaac accgatcctc caaacttccg 1500
tggccagaat ggatgggagt gatgcatggc tatgaaattg aatttgtctt tggtttacct 1560
ctggaaagaa gagataatta cacaaaagcc gaggaaattt tgagtagatc catagtgaag 1620
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<210> 17
 <211> 574
 <212> PRT
 <213> Homo sapiens

<400> 17

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Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro
			20					25						30	
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser
			35				40							45	
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
			50			55					60				
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
65					70					75					80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100					105						110	
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
			115				120						125		
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
			130			135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145					150					155					160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170					175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185						190	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
			195				200						205		
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
			210			215					220				
Gly	Ser	Phe	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225				230						235					240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
				245					250					255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile

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<210> 18
<211> 574
<212> PRT
<213> Homo sapiens
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<400> 18
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Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro
20 25 30
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser
35 40 45

Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
50						55					60				
Cys	Cys	Gln	Asn	Ile	Gly	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
65				70						75					80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100						105				110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
		115					120					125			
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
	130					135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145				150						155					160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170					175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
		195					200					205			
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210					215					220				
Gly	Ser	Phe	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225				230						235					240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
				245					250					255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
			260					265					270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val
		275					280					285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
	290					295					300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305				310						315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly
				325					330					335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340					345					350		
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser
		355					360					365			
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn
	370					375					380				
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys
385				390						395					400
Pro	Ala														

465		470		475		480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr						
		485		490		495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr						
		500		505		510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys						
		515		520		525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys						
		530		535		540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln						
545		550		555		560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu						
		565		570		

<210> 19
 <211> 574
 <212> PRT
 <213> Homo sapiens

<400> 19

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met																			
1				5				10											15
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro																			
			20					25											30
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser																			
			35					40											45
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser																			
			50					55											60
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu																			
65								70											75
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn																			
								85											90
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp																			
			100																105
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr																			
			115																120
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met																			
			130																135
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro																			
145																			150
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln																			
																			165
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val																			
			180																185
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu																			
			195																200
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser																			
			210																215
Gly Ser Phe Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg																			
225																			230
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn																			
																			245
																			250
																			255

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<210> 20
<211> 574
<212> PRT
<213> Homo sapiens
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<400> 20
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20 25 30
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser

	35				40				45						
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
50					55					60					
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
65					70					75					80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100						105				110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
		115					120						125		
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
130						135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145					150					155					160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170					175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
		195					200					205			
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
210						215					220				
Gly	Ser	Phe	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225				230						235					240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
				245					250					255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
			260					265					270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val
		275					280					285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
290						295					300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310					315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly
				325					330					335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340					345					350		
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser
		355					360					365			
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn
370						375					380				
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys
385					390					395					400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala
				405					410					415	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu
		420						425					430		
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu
		435				440						445			
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser
450						455					460				

TOP SECRET

Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro
465					470					475					480
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr
				485					490					495	
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr
			500					505					510		
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys
		515				520						525			
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Thr	Glu	Trp	Glu	Trp	Lys
	530					535					540				
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln
545				550						555					560
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu		
			565						570						

<210> 21

<211> 574

<212> PRT

<213> Equus caballus

<400> 21

Glu 1	Glu	Asp	Ile	Ile	Ile	Thr	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met
Asn	Leu	Pro	Val	Leu	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser
Leu	Thr	Lys	Trp	Ser	Asn	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
Cys 65	Tyr	Gln	Asn	Thr	Asp	Gln	Ser	Phe	Pro	Gly	Phe	Leu	Gly	Ser	Glu
Met	Trp	Asn	Pro	Asn	Thr	Glu	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Met	Ile	Trp
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	Pro	Val	Tyr
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
Asn 145	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Ser	Glu	Asn	Pro
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Arg	Ser	Val
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
Leu	Ser	Pro	Arg	Ser	Gln	Pro	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
Gly 225	Ser	Ser	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
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<210> 22
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<212> PRT
<213> Felis catus
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Asn Leu Pro Val Leu Asp Gly Thr Val Thr Ala Phe Leu Gly Ile Pro
20 25 30

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	35					40					45				
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
	50					55					60				
Cys	Tyr	Gln	Asn	Ala	Asp	Gln	Ser	Phe	Pro	Gly	Phe	Pro	Gly	Ser	Glu
65					70					75					80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Thr	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Met	Ile	Trp
			100					105					110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	Pro	Val	Tyr
		115					120					125			
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
	130					135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145					150					155					160
Glu	Val	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170						175
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Gly	Ser	Val	Ser	Leu	His	Leu
		195					200					205			
Leu	Ser	Pro	Arg	Ser	Gln	Pro	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210					215					220				
Gly	Ser	Ser	Asn	Ala	Pro	Trp	Ala	Val	Met	Ser	Leu	Asp	Glu	Ala	Lys
225					230					235					240
Asn	Arg	Thr	Leu	Thr	Leu	Ala	Lys	Phe	Ile	Gly	Cys	Ser	Lys	Glu	Asn
				245					250					255	
Asp	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
			260					265					270		
Leu	Leu	Asn	Glu	Leu	Leu	Val	Val	Pro	Ser	Asp	Thr	Leu	Leu	Ser	Val
		275					280					285			
Asn	Phe	Gly	Pro	Val	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
	290					295					300				
Thr	Leu	Leu	Gln	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310						315				320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly
				325					330					335	
Phe	Ser	Lys	Asp	Asn	Asp	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340					345					350		
Gly	Leu	Lys	Ile	Tyr	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Arg	Glu	Ala
		355					360					365			
Ile	Leu	Phe	Tyr	Tyr	Val	Asp	Leu	Leu	Asp	Asp	Gln	Arg	Ala	Glu	Lys
		370				375					380				
Tyr	Arg	Glu													

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Arg Ser Ile Met Asn Tyr Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro				
465		470		480
Asn Gly Thr Gln Asn Asn Ser Thr Arg Trp Pro Ala Phe Arg Ser Thr				
	485		490	495
Asp Gln Lys Tyr Leu Thr Leu Asn Ala Glu Ser Pro Lys Val Tyr Thr				
	500		505	510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Leu Phe Phe Pro Lys				
	515		520	525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Arg Glu Trp Arg				
	530		535	540
Ala Gly Phe Tyr Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln				
545		550		555
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Ala Gly Leu				560
	565		570	

<210> 23
 <211> 574
 <212> PRT
 <213> Rattus sp.

<400> 23

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Tyr Ala Gln Pro Pro Leu Gly Ser Leu Arg Phe Lys Lys Pro Gln Pro				
	35		40	45
Leu Asn Lys Trp Pro Asp Val Tyr Asn Ala Thr Lys Tyr Ala Asn Ser				
	50		55	60
Cys Tyr Gln Asn Ile Asp Gln Ala Phe Pro Gly Phe Gln Gly Ser Glu				
65		70		75
Met Trp Asn Pro Asn Thr Asn Leu Ser Glu Asp Cys Leu Tyr Leu Asn				
	85		90	95
Val Trp Ile Pro Val Pro Lys Pro Lys Asn Ala Thr Val Met Val Trp				
	100		105	110
Val Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu Pro Val Tyr				
	115		120	125
Asp Gly Lys Phe Leu Thr Arg Val Glu Arg Val Ile Val Val Ser Met				
	130		135	140
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Phe Pro Gly Asn Ser				
145		150		155
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln				
	165		170	175
Trp Ile Gln Arg Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val				
	180		185	190
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu				
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Leu Cys Pro Gln Ser Tyr Pro Leu Phe Thr Arg Ala Ile Leu Glu Ser				
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Gly Ser Ser Asn Ala Pro Trp Ala Val Lys His Pro Glu Glu Ala Arg				
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694439-000101

Asn	Arg	Thr	Leu	Thr	Leu	Ala	Lys	Phe	Ile	Gly	Cys	Ser	Lys	Glu	Asn		
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Glu	Lys	Glu	Ile	Ile	Thr	Cys	Leu	Arg	Ser	Lys	Asp	Pro	Gln	Glu	Ile		
			260					265					270				
Leu	Leu	Asn	Glu	Lys	Leu	Val	Leu	Pro	Ser	Asp	Ser	Ile	Arg	Ser	Ile		
		275					280					285					
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	His		
	290					295					300						
Thr	Leu	Leu	Gln	Leu	Gly	Lys	Val	Lys	Thr	Ala	Gln	Ile	Leu	Val	Gly		
305					310					315					320		
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly		
			325					330						335			
Phe	Ser	Lys	Asp	Asn	Asp	Ser	Leu	Ile	Thr	Arg	Arg	Glu	Phe	Gln	Glu		
			340				345						350				
Gly	Leu	Asn	Met	Tyr	Phe	Pro	Gly	Val	Ser	Ser	Leu	Gly	Lys	Glu	Ala		
		355					360					365					
Ile	Leu	Phe	Tyr	Tyr	Val	Asp	Trp	Leu	Gly	Asp	Gln	Thr	Pro	Glu	Val		
	370					375					380						
Tyr	Arg	Glu	Ala	Phe	Asp	Asp	Ile	Ile	Gly	Asp	Tyr	Asn	Ile	Ile	Cys		
385					390					395					400		
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ala	Glu	Leu	Glu	Ile	Asn	Ala		
				405					410					415			
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu		
			420					425					430				
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu		
		435					440					445					
Pro	Leu	Glu	Arg	Arg	Val	Asn	Tyr	Thr	Arg	Ala	Glu	Glu	Ile	Phe	Ser		
	450					455					460						
Arg	Ser	Ile	Met	Lys	Thr	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	His	Pro		
465					470					475					480		
Asn	Gly	Thr	Gln	Gly	Asn	Ser	Thr	Val	Trp	Pro	Val	Phe	Thr	Ser	Thr		
				485					490					495			
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Lys	Ser	Lys	Ile	Asn	Ser		
			500					505					510				
Lys	Leu	Arg	Ala	Pro	Gln	Cys	Gln	Phe	Trp	Arg	Leu	Phe	Phe	Pro	Lys		
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Val	Leu	Glu	Ile	Thr	Gly	Asp	Ile	Asp	Glu	Arg	Glu	Gln	Glu	Trp	Lys		
	530					535					540						
Ala	Gly	Phe	His	Arg	Trp	Ser	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln		
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Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Thr	Cys	Thr	Asp	Leu				
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<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> human butyrylcholinesterase variant

<400> 24

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34

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